

SEQUENCE LISTING

<110> Cahoon, Edgar B.
Kinney, Anthony
Klein, Thodore
Lee, Jian Ming
Pearlstein, Richard
Rafalski, J. Antoni
Shen, Jennie
Thorpe, Cathy
Tingey, Scott
Weng, Zude

<120> Plant Lipoxygenases

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<150> 09/501,422
<151> 2000-02-09

<150> 60/119,597
<151> 1999-02-10

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 gaagaagatc aaaggacgg tggttcttat gagaagcaat gttttggact tcaccgaatt 180
 tcattcctca cttcttgacg gcgtcactga gctctggc ggcggaaattt cattgcaact 240
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 accagtgagt tcttcctcaa gtctgttaact ccnggaggat ttccctggcnt tggaagggtcc 480
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Gly Asp Leu Ala Gly Ser Val Ile Asn Ala Gly Gly Asn Ile Val Gly
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Arg Val Thr Asn Ile Gly Gly Lys Ile Lys Gly Thr Val Val Leu
 35 40 45

Met Arg Ser Asn Val Leu Asp Phe Thr Glu Phe His Ser Ser Leu Leu
 50 55 60

Asp Gly Val Thr Glu Leu Leu Gly Gly Gly Ile Ser Leu Gln Leu Ile
65 70 75 80

Ser Ala Thr His Ala Ser Asn Asp Ser Arg Gly Lys Val Gly Lys Gly
85 90 95

Ala Phe Leu Glu Arg Trp Leu Thr Ser Val Pro Pro Leu Phe Ala Gly
100 105 110

Glu Ser Val Phe Gln Val Asn Phe Leu Gly Arg Glu Leu Trp Asp Phe
115 120 125

Gln Gly Ala Phe Phe Ile Lys Asn Gly His Thr Ser Glu Phe Phe Leu
130 135 140

Lys Ser Val Thr Pro Gly Gly Phe Pro Gly Xaa Lys Val His Phe Asp
145 150 155 160

Cys Asn Ser Xaa Val Xaa Pro Ser Arg Arg
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atccttagga aagatggac tttgatgccca ttagccattg agctaagcct gcccaaccca 180
agaggagatg aatatggtgc catatgcaaa gtctacaccc cggctcaaca tggtgttagaa 240
gctccctt ggcagcttgc ttaaggctat gtcgtggta acgactctt tattcacgaa 300
tccgtccagt cattgggaaa gaacacgcaa gcagtgattt agcattttgtt atcgcgacaa 360
acagacactt agcgtacttt atccgatcaa aagttgttca ccctcatttt ccgagacacg 420
attaacatta tgcacatcgcaa ggaagtacta atcacgcggg ttgagttt gagaacttt 480
tcacatcnna gtanacagga gattcctccg caattacaag aatggnttt acgacantcc 540
tcccctggnc tattaaaggg gattgcgtaa gntataagaa aaccgtctcg caccaaaaga 600
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Asp Ser Leu Met Pro Tyr Leu Gly Arg Ile Asn Thr Thr Thr Lys
20 25 30

Thr Tyr Ala Ser Arg Thr Leu Leu Ile Leu Arg Lys Asp Gly Thr Leu
35 40 45

Met Pro Leu Ala Ile Glu Leu Ser Leu Pro Asn Pro Arg Gly Asp Glu
50 55 60

Tyr Gly Ala Ile Cys Lys Val Tyr Thr Pro Ala Gln His Gly Val Glu
65 70 75 80

Ala Ser Leu Trp Gln Leu Ala Xaa Ala Tyr Val Val Val Asn Asp Ser
85 90 95

Cys Ile His Glu Ser Val
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ggngacggcg tcggnggagg cgtcgccgac catcgccag atgtacttcc agcgcgcccgt 180
cgacgacatc ggccacccctcc tcggcaagac gctgctgctc gagctcgta gctccgagct 240
cgacgcaaaag tcgggcgtgg agaaaaacgcg ggtgacggcg tacgcgcaca agacgctgcg 300
ggagggccac tacgaggcg agttcaaggt gccgcgtcg ttcgggcccgg tgggcgcgg 360
gctgggtggag aacgagcacc acaaggaggt cttcatcaag gagatcaagc tcgtcaccgg 420
cggcgacagc agcaccggcg tcaccttgcg ctgcaactcc tgggtgcact ccaagttcg 480
caacccggag aagcgcatct tcttcaccct caagtcatc acgcgtccg acacgccc 540
ggggctggag gacctgagga agaaaagacct gcaggcgctg cgccggcagc ggcacggcga 600
gcgcaagggtg ttcgagcgcg tctacgacta cgacgtgtac aacgaactgg goga 654

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Glu Lys Thr Arg Val Thr Ala Tyr Ala His Lys Thr Leu Arg Glu Gly
20 25 30
His Tyr Glu Ala Glu Phe Lys Val Pro Ala Ser Phe Gly Pro Val Gly
35 40 45
Ala Val Leu Val Glu Asn Glu His His Lys Glu Val Phe Ile Lys Glu
50 55 60
Ile Lys Leu Val Thr Gly Gly Asp Ser Ser Thr Ala Val Thr Phe Asp
65 70 75 80
Cys Asn Ser Trp Val His Ser Lys Phe Asp Asn Pro Glu Lys Arg Ile
85 90 95
Phe Phe Thr Leu Lys Ser Tyr Leu Pro Ser Asp Thr Pro Lys Gly Leu
100 105 110
Glu Asp Leu Arg Lys Lys Asp Leu Gln Ala Leu Arg Gly Asp Gly His
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Gly Glu Arg Lys Val Phe Glu Arg Val Tyr Asp Tyr Asp Val Tyr Asn
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Glu Leu Gly
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 cacatcacat cggcaggcgaa gggacggagc gagcaaggaa gcccattccac cagccagcca 180
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 ggtcgccggac cggctgacgg gaaagaacaa ggaggcgtgg agcgaggcga agatccgcgg 300
 cacggtgagg ctggtaaga aggaggtgct ggacgtcggc gacttcaacg cctcgctcct 360
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 gaggcggtg gtcgctcaa gtcacggcgg acggggagan cgtgtacccgg gtgaagcttc 540
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Arg Ser Ser Thr Leu Pro Tyr Thr Pro Ala Leu Cys Leu Pro Phe Pro
 20 25 30

Cys Leu Ala Ser Leu Ile Ala Gly Thr Ser His Arg Gln Ala Arg Asp
 35 40 45

Gly Ala Ser Arg Glu Ala His Pro Pro Ala Ser His Arg Val Pro Glu
 50 55 60

Lys Arg Arg Ala Arg Lys Gly Glu Xaa Ala Xaa Met Phe Trp His Gly
 65 70 75 80

Val Ala Asp Arg Leu Thr Gly Lys Asn Lys Glu Ala Trp Ser Glu Gly
 85 90 95

Lys Ile Arg Gly Thr Val Arg Leu Val Lys Lys Glu Val Leu Asp Val
 100 105 110

Gly Asp Phe Asn Ala Ser Leu Leu Asp Gly Val His Arg Ile Leu Gly
115 120 125

Trp Asp Asp Gly Val Ala Phe Ser Ser Ser Ala Pro Pro Arg Ala Thr
130 135 140

Pro Ala Thr Gly Ala Val Ala Arg Trp Gly Arg Arg Arg Thr Trp Arg
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Arg Arg Trp Cys Arg Ser Ser His Gly Gly Arg Gly
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 cttggacgtc accagcatcg cccgctccct cctcgacggc gtcggcgagt tcctcggccg 240
 cggcgtcacc tgccagctta tcaagctccac cgtcgctcgac cctaacaacg gcaaccgggg 300
 gaagttgggc gcggaggcgca gcctggagaca gtggctgctg aacccggccg cgcttctgtc 360
 cagcgagaac cagttcccgca tcaccttcga ctgggaggtg gagaaggcagg gcatcccgaa 420
 ccccatcatc gtcaagaaca accacgcctn cgagncttc ctcaagacca tcaccctcaa 480
 cgacgtcccc ggcacgggac catcgcttc gtgcggcaact catggatcta cccgcagtcc 540
 aagtaccgct acaaccgcgt cttttctcc aacgacacgt accttcccaa gccagatgcc 600
 ggcggcgctg aagcctaccg ngacgacacgc ttccggaaacc tgagggggca cgaccagcaa 660
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His Leu Lys Gly Asn Val Val Leu Val Arg Lys Thr Val Leu Gly Leu
35 40 45

Asp Val Thr Ser Ile Ala Gly Ser Leu Leu Asp Gly Val Gly Glu Phe
50 55 60

Leu Gly Arg Gly Val Thr Cys Gln Leu Ile Ser Ser Thr Val Val Asp
65 70 75 80

Pro Asn Asn Gly Asn Arg Gly Lys Leu Gly Ala Glu Ala Ser Leu Glu
85 90 95

Gln Trp Leu Leu Asn Pro Pro Pro Leu Leu Ser Ser Glu Asn Gln Phe
100 105 110

Arg Val Thr Phe Asp Trp Glu Val Glu Lys Gln Gly Ile Pro Gly Ala
115 120 125

Ile Ile Val Lys Asn Asn His Ala Xaa Glu Xaa Phe Leu Lys Thr Ile
130 135 140

Thr Leu Asn Asp Val Pro Gly Thr Gly Pro Ser Ser Ser Ser Pro Thr
145 150 155 160

His Gly Ser Thr Arg Ser Pro Ser Thr Ala Thr Thr Ala Ser Ser Ser
165 170 175

Pro Thr Thr Arg Thr Phe Pro Ser Gln Met Pro Ala Ala Leu Lys Pro
180 185 190

Thr Xaa Thr Thr Ala Ser Gly Thr Xaa Thr Ile Val Phe Val Ala Asn
195 200 205

Ser Trp Ile Tyr Pro Gln Ser Lys Tyr Arg Tyr Asn Arg Val Phe Phe
210 215 220

Ser Asn Asp Thr Tyr Leu Pro Lys Pro Asp Ala Gly Gly Ala Glu Ala
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Tyr Arg Asp Asp Ser Phe Arg Asn Leu Arg Gly Asp Asp Gln Gln Gly
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Pro Xaa Gln Glu His Glu
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<212> DNA

<213> Momordica charantia

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tcggcgggaa gaagatcaa gggacgggtgg ttcttatgag aagcaatgtt ttggacttca 180
ccgaatttca ttccctcaatt cttgacggcg tcactgagct cttggggccgc ggaatttcat 240
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20 25 30

Arg Val Thr Asn Ile Gly Gly Lys Lys Ile Lys Gly Thr Val Val Leu
35 40 45

Met Arg Ser Asn Val Leu Asp Phe Thr Glu Phe His Ser Ser Leu Leu
 50 55 60

Asp Gly Val Thr Glu Leu Leu Gly Gly Ile Ser Leu Gln Leu Ile
 65 70 75 80

Ser Ala Thr His Ala Ser Asn Asp Ser Arg Gly Lys Val Gly Lys Gly
 85 90 95

Ala Phe Leu Glu Arg Trp Leu Thr Ser Val Pro Pro Leu Phe Ala Gly
 100 105 110

Glu Ser Val Phe Gln Val Asn Phe Asp Trp Glu Glu Asn Phe Gly Phe
 115 120 125

Pro Gly Ala Phe Phe Ile Lys Asn Gly His Thr Ser Glu Phe Phe Leu
 130 135 140

Lys Ser Val Thr Leu Glu Asp Val Pro Gly Phe Gly Arg Val His Phe
 145 150 155 160

Asp Cys Asn Ser Trp Val Tyr Pro Ser Arg Arg Tyr Lys Lys Asp Arg
 165 170 175

Ile Phe Phe Ala Asn His Thr Cys Leu Pro Ile Asp Thr Pro Asp Ser
 180 185 190

Leu Arg Lys Tyr Arg Glu Glu Glu Leu Leu Asn Leu Arg Gly Asp Gly
 195 200 205

Thr Gly Glu Arg Lys Glu Trp Asp Arg Ile Tyr Asp Tyr Asp Val Tyr
 210 215 220

Asn Asp Leu Cys Asp Pro Asn Gly Gly Pro Asn Leu Val Arg Pro Ile
 225 230 235 240

Leu Gly Gly Ser Asp Gln Tyr Pro Tyr Pro Arg Arg Gly Arg Thr Gly
 245 250 255

Arg Pro Pro Ala Arg Lys Asp His Lys Tyr Glu Ser Arg Leu Ser Asp
 260 265 270

Val Met Ser Leu Asn Ile Tyr Val Pro Arg Asp Glu Asn Phe Gly His
 275 280 285

Leu Lys Met Ala Asp Phe Leu Gly Asn Thr Leu Lys Val Leu Ser Thr
 290 295 300

Ser Ile Gln Pro Gly Leu Glu Ser Ile Phe Asp Ser Thr Pro Gly Glu
 305 310 315 320

Phe Asp Lys Phe Lys Glu Val Asp Asp Leu Phe Glu Arg Gly Phe Pro
 325 330 335

Ile Pro Leu Asn Ile Phe Lys Asn Leu Thr Glu Asp Leu Ala Pro Pro
 340 345 350

Leu Phe Lys Ala Phe Leu Arg Ser Asp Gly Glu Arg Phe Leu Lys Tyr
 355 360 365

Pro Thr Pro Gln Val Ile Lys Asp Asn Lys Leu Gly Trp Arg Thr Asp
 370 375 380
 Glu Glu Phe Ala Arg Glu Met Ile Ala Gly Val Asn Pro Leu Ile Ile
 385 390 395 400
 Arg Arg Leu Glu Val Phe Pro Pro Leu Ser Lys Leu Asp Pro His Val
 405 410 415
 Tyr Gly Asn Gln Asn Ser Thr Met Thr Glu Glu Gln Ile Lys His Gly
 420 425 430
 Leu Asp Gly Leu Thr Val Asp Glu Ala Ile Lys Glu Asn Lys Leu Tyr
 435 440 445
 Ile Leu Asp His His Asp Ala Leu Met Pro Tyr Leu Arg Arg Ile Asn
 450 455 460
 Ser Thr Ser Thr Lys Thr Tyr Ala Thr Arg Thr Leu Leu Phe Leu Lys
 465 470 475 480
 Asp Asp Ser Thr Leu Lys Pro Leu Ala Ile Glu Leu Ser Leu Pro His
 485 490 495
 Pro Gln Gly Asp Glu His Gly Ala Ile Ser Lys Leu Tyr Phe Pro Ala
 500 505 510
 Glu Gly Arg Val Glu Ser Ala Ile Trp Gln Leu Ala Lys Ala Tyr Val
 515 520 525
 Ala Val Asn Asp Ser Gly Tyr His Gln Leu Asn Ser His Trp Leu His
 530 535 540
 Thr His Ala Val Leu Glu Pro Phe Val Ile Thr Thr His Arg Arg Leu
 545 550 555 560
 Ser Val Leu His Pro Ile His Lys Leu Leu Ala Pro His Tyr Lys Asp
 565 570 575
 Thr Met Phe Ile Asn Ala Ser Ala Arg Gln Val Leu Ile Asn Ala Gly
 580 585 590
 Gly Leu Ile Glu Ser Thr Gln Phe Pro Ala Lys Tyr Ala Met Glu Leu
 595 600 605
 Ser Ser Tyr Ile Tyr Lys Glu Trp Lys Phe Pro Asp Glu Ala Leu Pro
 610 615 620
 Thr Asn Leu Ile Lys Arg Gly Val Ala Ile Glu Asp Ser Gly Ser Pro
 625 630 635 640
 His Gly Val Arg Leu Leu Ile Asn Asp Tyr Pro Phe Ala Val Asp Gly
 645 650 655
 Leu Glu Ile Trp Ser Ala Ile Lys Thr Trp Val Thr Asp Tyr Cys Ser
 660 665 670
 Leu Tyr Tyr Lys Asp Asp Asp Ala Ile Arg Asn Asp Val Glu Leu Gln
 675 680 685

Ser Trp Trp Lys Glu Leu Arg Glu Lys Gly His Thr Asp Lys Lys Asp
 690 695 700
 Glu Pro Trp Trp Pro Lys Met Gln Thr Phe Ser Glu Leu Ile Glu Ser
 705 710 715 720
 Cys Thr Ile Ile Ile Trp Ile Ser Ser Ala Leu His Ala Ala Val Asn
 725 730 735
 Phe Gly Gln Tyr Pro Tyr Gly Gly Tyr Val Pro Asn Arg Pro Thr Thr
 740 745 750
 Ser Arg Arg Phe Met Pro Glu Val Gly Thr Ala Glu Tyr Lys Glu Val
 755 760 765
 Glu Ser Asn Pro Glu Lys Ala Phe Leu Arg Thr Ile Ser Ser Gln Ile
 770 775 780
 Val Ala Leu Leu Gly Leu Ser Ile Ile Glu Ile Leu Ser Lys His Ala
 785 790 795 800
 Ser Asp Glu Val Tyr Leu Gly Gln Arg Ala Ser Ile Glu Trp Thr Ser
 805 810 815
 Asp Lys Ser Ala Ile Glu Ala Phe Glu Lys Phe Gly Lys Glu Leu Phe
 820 825 830
 Glu Val Glu Asp Arg Ile Met Arg Arg Asn Gln Asp Val Asn Leu Lys
 835 840 845
 Asn Arg Ala Gly Pro Val Asn Met Pro Tyr Thr Leu Leu Val Pro Ser
 850 855 860
 Ser Thr Glu Gly Leu Thr Gly Arg Gly Ile Pro Asn Ser Ile Ser Ile
 865 870 875 880

<210> 13
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 <213> Impatiens balsamia

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 tgagaatacg ttttcacat caaagtatac catggagatg tcattccgaa tttacaagaa 540
 ttggattttc accgaccagt ctctcccggt ggaccttatt aaaaggggga ttgcggttaa 600
 ggtatgataaa gaaaaacgcg gtcttcgcct actcatagag gattaccgt atgcgggtga 660
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<211> 445
<212> PRT
<213> Impatiens balsamia

<400> 14
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20 25 30
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35 40 45
Thr Leu Met Pro Leu Ala Ile Glu Leu Ser Leu Pro Asn Pro Arg Gly
50 55 60
Asp Glu Tyr Gly Ala Ile Cys Lys Val Tyr Thr Pro Ala Gln His Gly
65 70 75 80
Val Glu Ala Ser Leu Trp Gln Leu Ala Lys Ala Tyr Val Val Val Asn
85 90 95
Asp Ser Gly Ile His Glu Leu Val Ser His Trp Leu Asn Thr His Ala
100 105 110
Val Ile Glu Pro Phe Val Ile Ala Thr Asn Arg Gln Leu Ser Val Leu
115 120 125
His Pro Ile Gln Lys Leu Leu His Pro His Phe Arg Asp Thr Met Asn
130 135 140
Ile Asn Ala Ile Ala Arg Asn Val Leu Ile Asn Ala Gly Gly Val Ile
145 150 155 160
Glu Asn Thr Phe Phe Thr Ser Lys Tyr Ser Met Glu Met Ser Ser Ala
165 170 175
Ile Tyr Lys Asn Trp Ile Phe Thr Asp Gln Ser Leu Pro Val Asp Leu
180 185 190
Ile Lys Arg Gly Ile Ala Val Lys Asp Asp Lys Glu Lys Arg Gly Leu
195 200 205
Arg Leu Leu Ile Glu Asp Tyr Pro Tyr Ala Val Asp Gly Leu Glu Ile
210 215 220
Trp Phe Ala Ile Lys Thr Trp Val Glu Asp Tyr Cys Asp Phe Tyr Tyr
225 230 235 240

Lys Gly Asp Glu Ala Val Lys Asn Asp Thr Glu Leu Gln Ala Trp Trp
245 250 255

Lys Glu Leu Lys Glu Val Gly His Gly Asp Lys Arg Asn Glu Pro Trp
260 265 270

Trp Pro Lys Met Glu Thr Arg Lys Asp Leu Leu Glu Thr Cys Thr Ile
275 280 285

Ile Ile Trp Val Ala Ser Ala Leu His Ala Ala Leu Asn Phe Gly Gln
290 295 300

Tyr Pro Tyr Gly Gly Tyr His Pro Asn Arg Pro Thr Asn Ser Arg Arg
305 310 315 320

Leu Met Pro Glu Val Gly Ser Pro Glu Phe Glu Glu Leu Lys Thr Asn
325 330 335

Pro Asp Gln Ile Leu Leu Lys Thr Leu Ser Ser Lys Ala Gln Thr Leu
340 345 350

Leu Glu Val Ala Ile Ile Glu Ile Leu Ser Arg His Thr Ser Asp Glu
355 360 365

Val Tyr Leu Gly Gln Arg Asp Thr Pro Glu Trp Thr Lys Asp Glu Glu
370 375 380

Pro Leu Lys Ala Phe Asp Lys Phe Gly Lys Lys Leu Ala Glu Ile Glu
385 390 395 400

Val Arg Ile Ile Glu Met Asn Asn Asp Glu Ser Leu Lys Asn Arg Asn
405 410 415

Gly Pro Val Lys Ile Pro Tyr Thr Leu Leu Phe Pro Thr Ser Ser Ser
420 425 430

Gly Leu Thr Gly Lys Gly Ile Ser Asn Ser Val Ser Ile
435 440 445

<210> 15

<211> 3134

<212> DNA

<213> Zea mays

<400> 15

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 <212> PRT
 <213> Zea mays

<400> 16
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Glu Val Leu Asp Val Gly Asp Phe Asn Ala Ser Leu Leu Asp Gly Val
 35 40 45

His Arg Ile Leu Gly Trp Asp Asp Gly Val Ala Phe Gln Leu Val Ser
 50 55 60

Ala Thr Ala Ala Asp Pro Ser Asn Gly Gly Arg Gly Lys Val Gly Lys
 65 70 75 80

Ala Ala His Leu Glu Glu Ala Val Val Ser Leu Lys Ser Thr Ala Asp
 85 90 95
 Gly Glu Thr Val Tyr Arg Val Ser Phe Glu Trp Asp Glu Ser Gln Gly
 100 105 110
 Ile Pro Gly Ala Val Leu Val Arg Asn Leu Gln His Ala Glu Phe Phe
 115 120 125
 Leu Lys Thr Leu Thr Leu Glu Gly Val Pro Gly Lys Gly Thr Val Val
 130 135 140
 Phe Val Ala Asn Ser Trp Val Tyr Pro His Lys Leu Tyr Ser Gln Glu
 145 150 155 160
 Arg Ile Phe Phe Ala Asn Asp Thr Tyr Leu Pro Ser Lys Met Pro Ala
 165 170 175
 Ala Leu Val Pro Tyr Arg Gln Asp Glu Leu Lys Ile Leu Arg Gly Asp
 180 185 190
 Asp Asn Pro Gly Pro Tyr Gln Glu His Asp Arg Val Tyr Arg Tyr Asp
 195 200 205
 Tyr Tyr Asn Asp Leu Gly Asp Pro Asp Lys Gly Glu Glu His Ala Arg
 210 215 220
 Pro Ile Leu Gly Gly Ser Gln Glu His Pro Tyr Pro Arg Arg Cys Arg
 225 230 235 240
 Thr Gly Arg His Pro Thr Lys Lys Asp Pro Asn Ser Glu Ser Arg Leu
 245 250 255
 Phe Leu Leu Asn Leu Asn Ile Tyr Val Pro Arg Asp Glu Arg Phe Gly
 260 265 270
 His Leu Lys Met Ser Asp Phe Leu Gly Tyr Ser Leu Lys Thr Ile Ile
 275 280 285
 Glu Ala Val Leu Pro Thr Leu Gly Thr Phe Val Asp Asp Thr Pro Lys
 290 295 300
 Glu Phe Asp Ser Phe Glu Asp Ile Leu Gly Leu Tyr Glu Leu Gly Pro
 305 310 315 320
 Glu Ala Pro Asn Asn Pro Leu Ile Ala Glu Ile Arg Lys Lys Ile Pro
 325 330 335
 Ser Glu Phe Leu Arg Ser Ile Leu Pro Asn Gly Ser His Asp His Pro
 340 345 350
 Leu Lys Met Pro Leu Pro Asn Val Ile Lys Ser Asp Val Leu Lys Lys
 355 360 365
 Ala Pro Glu Phe Lys Phe Gly Trp Arg Thr Asp Glu Glu Phe Ala Arg
 370 375 380
 Glu Thr Leu Ala Gly Val Asn Pro Val Ile Ile Lys Arg Leu Thr Glu
 385 390 395 400

Phe Pro Ala Lys Ser Thr Leu Asp Pro Arg Gln Tyr Gly Asp His Thr
 405 410 415
 Ser Lys Ile Thr Glu Ala His Ile Arg His Asn Met Gly Gly Leu Ser
 420 425 430
 Val Gln Asn Ala Leu Arg Asn Lys Arg Leu Phe Ile Leu Asp His His
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 Asp His Phe Met Pro Tyr Leu Asp Glu Ile Asn Glu Leu Glu Gly Asn
 450 455 460
 Phe Ile Tyr Ala Ser Arg Thr Leu Leu Phe Leu Lys Asp Asp Gly Thr
 465 470 475 480
 Leu Lys Pro Leu Ala Ile Glu Leu Ser Leu Pro His Pro Asp Gly Gln
 485 490 495
 Gln Arg Gly Ala Val Ser Lys Val Tyr Thr Pro Ala His Thr Gly Val
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 Glu Gly His Val Trp Gln Leu Ala Lys Ala Tyr Ala Cys Val Asn Asp
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 Ser Ala Trp His Gln Leu Ile Ser His Trp Leu Asn Thr His Ala Val
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 Ile Glu Pro Phe Val Ile Ala Thr Asn Arg Gln Leu Ser Val Val His
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 Pro Val His Lys Leu Leu Ser Pro His Tyr Arg Asp Thr Leu Asn Ile
 565 570 575
 Asn Ala Leu Ala Arg Gln Thr Leu Ile Asn Ala Gly Gly Val Phe Glu
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 Arg Thr Val Phe Pro Ala Lys Tyr Ala Leu Gly Met Ser Ala Asp Val
 595 600 605
 Tyr Lys Ser Trp Asn Phe Asn Glu Gln Ala Leu Pro Ala Asp Leu Val
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 Lys Arg Gly Val Ala Val Pro Asp Gln Ser Ser Pro Tyr Gly Val Arg
 625 630 635 640
 Leu Leu Ile Lys Asp Tyr Pro Tyr Ala Val Asp Gly Leu Val Ile Trp
 645 650 655
 Trp Ala Ile Glu Arg Trp Val Lys Glu Tyr Leu Asp Ile Tyr Tyr Pro
 660 665 670
 Asn Asp Gly Glu Leu Gln Arg Asp Val Glu Leu Gln Ala Trp Trp Lys
 675 680 685
 Glu Val Arg Glu Glu Ala His Gly Asp Leu Lys Asp Arg Asp Trp Trp
 690 695 700
 Pro Arg Met Asp Thr Val Gln Gln Leu Ala Arg Ala Cys Thr Thr Ile
 705 710 715 720

Ile Trp Val Ala Ser Ala Leu His Ala Ala Val Asn Phe Gly Gln Tyr
725 730 735

Pro Tyr Ala Gly Tyr Leu Pro Asn Arg Pro Thr Ala Ser Arg Arg Pro
740 745 750

Met Pro Glu Pro Gly Ser His Asp Tyr Lys Lys Leu Gly Ala Gly Gln
755 760 765

Lys Glu Ala Asp Met Val Phe Ile Arg Thr Ile Thr Ser Gln Phe Gln
770 775 780

Thr Ile Leu Gly Ile Ser Leu Ile Glu Ile Leu Ser Lys His Ser Ser
785 790 795 800

Asp Glu Val Tyr Leu Gly Gln Arg Asp Glu Pro Asp Arg Trp Thr Ser
805 810 815

Asp Ala Lys Ala Leu Asp Ala Phe Lys Arg Phe Gly Ser Arg Leu Val
820 825 830

Gln Ile Glu Asn Arg Ile Lys Thr Met Asn Asp Ser Pro Asp Leu Lys
835 840 845

Asn Arg Lys Gly Pro Val Glu Met Pro Tyr Met Leu Leu Tyr Pro Asn
850 855 860

Thr Ser Asp Val Thr Gly Glu Lys Ala Glu Gly Leu Thr Ala Met Gly
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Ile Pro Asn Ser Ile Ser Ile
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<210> 17

<211> 1438

<212> DNA

<213> Zea mays

<400> 17

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<212> PRT
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<400> 18
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Gln Met Tyr Phe Gln Arg Ala Val Asp Asp Ile Gly Asp Leu Leu Gly
35 40 45

Lys Thr Leu Leu Leu Glu Leu Val Ser Ser Glu Leu Asp Ala Lys Ser
50 55 60

Gly Val Glu Lys Thr Arg Val Thr Ala Tyr Ala His Lys Thr Leu Arg
65 70 75 80

Glu Gly His Tyr Glu Ala Glu Phe Lys Val Pro Ala Ser Phe Gly Pro
85 90 95

Val Gly Ala Val Leu Val Glu Asn Glu His His Lys Glu Val Phe Ile
100 105 110

Lys Glu Ile Lys Leu Val Thr Gly Gly Asp Ser Ser Thr Ala Val Thr
115 120 125

Phe Asp Cys Asn Ser Trp Val His Ser Lys Phe Asp Asn Pro Glu Lys
130 135 140

Arg Ile Phe Phe Thr Leu Lys Ser Tyr Leu Pro Ser Asp Thr Pro Lys
145 150 155 160

Gly Leu Glu Asp Leu Arg Lys Lys Asp Leu Gln Ala Leu Arg Gly Asp
165 170 175

Gly His Gly Glu Arg Lys Val Phe Glu Arg Val Tyr Asp Tyr Asp Val
180 185 190

Tyr Asn Asp Leu Gly Asp Pro Asp Lys Asn Pro Ala His Gln Arg Pro
195 200 205

Val Leu Gly Gly Asn Lys Gln Tyr Pro Tyr Pro Arg Arg Cys Arg Thr
210 215 220

Gly Arg Pro Arg Thr Lys Lys Asp Pro Glu Thr Glu Met Arg Glu Gly
225 230 235 240

His Asn Tyr Val Pro Arg Asp Glu Gln Phe Ser Glu Val Lys Gln Leu
245 250 255

Thr Phe Gly Ala Thr Thr Leu Arg Ser Gly Leu His Ala Leu Leu Pro
 260 265 270
 Ala Leu Arg Pro Leu Leu Ile Asn Lys Lys Asp Leu Arg Phe Pro His
 275 280 285
 Phe Pro Ala Ile Asp Asp Leu Phe Ser Asp Gly Ile Pro Leu Pro Ala
 290 295 300
 Gln Thr Gly Phe Asp Ala Phe Arg Thr Val Val Pro Arg Met Val Lys
 305 310 315 320
 Leu Val Glu Asp Thr Thr Asp His Val Leu Arg Phe Glu Val Pro Glu
 325 330 335
 Met Ile Glu Arg Asp Arg Phe Ser Trp Phe Lys Asp Glu Glu Phe Ala
 340 345 350
 Arg Gln Thr Ile Ala Gly Leu Asn Pro Leu Cys Ile Gln Leu Leu Thr
 355 360 365
 Glu Phe Pro Ile Lys Ser Lys Leu Asp Pro Glu Val Tyr Gly Pro Ala
 370 375 380
 Glu Ser Ala Ile Thr Lys Glu Ile Leu Glu Lys Gln Met Asn Gly Ala
 385 390 395 400
 Leu Thr Val Glu Gln Ala Leu Ala Ala Lys Arg Leu Phe Ile Leu Asp
 405 410 415
 Tyr His Asp Val Phe Leu Pro Tyr Val His Lys Val Arg Glu Leu Gln
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 Asp Ala Thr Leu Tyr Ala Ser Arg Thr Ile Phe Phe Leu Thr Asp Leu
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 Gly Thr Leu Met Pro Leu Ala Ile Glu Leu Thr Arg Pro Lys Ser Pro
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<210> 19
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<220>
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Val Xaa Glu Pro Phe Val Ile Xaa Thr Xaa Arg Xaa Leu Ser Val Xaa
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His Pro Xaa Xaa Lys Leu Leu Xaa Pro His Xaa Xaa Asp Thr Xaa Xaa
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Ile Asn
50

<210> 20
<211> 32
<212> PRT
<213> CONSENSUS SEQUENCE

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<223> Xaa = Val or Ile

<220>
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<222> (5)
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<223> Xaa = Tyr or Phe

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<223> Xaa = Leu, Ile, Val, or His

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<223> Xaa = Pro or Leu

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<223> Xaa = Thr or Ser

<220>
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Tyr Pro Tyr Xaa Gly Xaa Xaa Asn Arg Pro Xaa Xaa Ser Arg Arg
20 25 30

<210> 21
<211> 8
<212> PRT
<213> CONSENSUS SEQUENCE

<400> 21
Gly Ile Pro Asn Ser Ile Ser Ile
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